Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.-2. (Canceled)

3. (Currently amended) A method for producing a plant ~~that does not contain a T-DNA~~, comprising (1) transforming a plant cell using Agrobacterium with [[(i)]] a desired polynucleotide flanked by at least one sequence of (a) 25 nucleotides in length ~~from a plant~~ that (b) promotes and facilitates integration of the desired polynucleotide into the plant genome and which (c) is not 100% identical to a T-DNA border, and wherein (d) the 25 nucleotide-long sequence comprises (i) a plant DNA sequence that comprises the consensus nucleotide sequence of any one of SEQ ID NOs. 47, 93, 113, 115, and 117, or (ii) a nucleotide sequence that has at least 70% sequence identity to the consensus sequence of (i); and ~~(ii) a marker gene;~~ (2) growing a plant from said transformed plant cell, which comprises in its genome the desired polynucleotide~~, wherein the desired polynucleotide comprises sequences that are native to the genome of the plant cell; (3) self-fertilizing, cross-fertilizing, or asexually propagating the transformed plant to produce progeny plants and (4) identifying a progeny plant that does not comprise the marker gene in its genome, but does comprise the desired polynucleotide in its genome, wherein the desired polynucleotide and the marker gene are each operably linked to genetic sequences that facilitate their expression~~.

4. (Canceled)

5. (Previously presented) The method of claim 3, wherein the plant cell is a cell of a monocotyledon or dicotyledon plant.

6.-12. (Canceled)

13. (Currently amended) A progeny plant, comprising a desired polynucleotide in its genome, wherein the desired polynucleotide comprises a sequence that is (a) 25 nucleotides in length, and which (b) comprises (i) the consensus nucleotide sequence of any one of SEQ ID NOs. 47, 93, 113, 115, and 117, or (ii) a nucleotide sequence that has at least 70% sequence identity to the consensus sequence of (i), wherein the sequence (c) promotes and facilitates integration of the desired polynucleotide into the plant genome and (d) is not 100% identical to a T-DNA border~~, is operably linked to 5-100 nucleotides of a plant sequence that promotes and facilitates integration of a polynucleotide to which it is linked into a plant genome, wherein the plant sequence does not have a nucleotide sequence identical to a T-DNA border~~.

14.-43. (Canceled)

44. (Currently amended) The method of claim 3, further comprising co-transforming the plant cell with a marker, wherein the desired polynucleotide and the marker are each in carrier DNAs, which are located in separate *Agrobacterium* vectors.

45. (Previously presented) The method of claim 44, wherein each vector is in a different *Agrobacterium* strain to the other vector.

46. (Previously presented) The method of claim 45, wherein the desired polynucleotide is located in a carrier DNA that is a P-DNA.

47. (Previously presented) The method of claim 44, wherein all of the vectors are in the same *Agrobacterium* strain.

48. (Previously presented) The method of claim 46, wherein the desired polynucleotide is operably linked to regulatory elements that are native to plants.

49. (Previously presented) The method of claim 44, wherein the vector that comprises the marker gene, further comprises a second marker gene.

50. (Previously presented) The method of claim 49, wherein the second marker gene encodes bacterial cytosine deaminase.

51. (Previously presented) The method of claim 3, wherein the marker gene is expressed for 1 to 10 days.

52. (Previously presented) The method of claim 3, wherein the marker gene is a herbicide resistance gene or an antibiotic resistance gene.

53. (Previously presented) The method of claim 3, wherein the desired polynucleotide comprises sequences that, when expressed in a plant, facilitate the down-regulation of expression of at least one of R1, polyphenol oxidase, and phosphorylase.

54. (Previously presented) The method of claim 44, wherein either or both of (i) the vector that comprises the marker gene further comprises a backbone integration marker gene, and (ii) the vector that comprises the desired polynucleotide further comprises a backbone integration marker gene, wherein the backbone integration marker gene is not located in the transfer-DNA.

55. (Previously presented) The method of claim 54, wherein the integration marker gene is a gene encoding isopentyltransferase.

56.-57 (Canceled)

58. (New) The method of claim 3, wherein the 25 nucleotide-long sequence comprises at least one point mutation in its consensus sequence.

59. (New) A progeny plant obtained from the plant of claim 3, wherein the progeny plant comprises the desired polynucleotide in its genome.